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Snake Venomics Display: An online toolbox for visualization of snake venomics data

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Abstract

With the introduction of powerful mass spectrometry equipment into the field of snake venom proteomics, a large body of venomics data is accumulating. To allow for better comparison between venom compositions from different snake species and to provide an online database containing this data, we devised the Venomics Display toolbox for visualization of venomics data on linear scales. This toolbox is freely available to be used online at https://tropicalpharmacology.com/tools/snake-venomics-display/ and allows researchers to visualize venomics data in a Relative Abundance (%) visualization mode and in an Absolute Abundance (mg) visualization mode, the latter taking venom yields into account. The curated venomics data for all snake species included in this database is also made available in a downloadable Excel file format. The Venomics Display toolbox represents a simple way of handling venomics data, which is better suited for large data sets of venom compositions from multiple snake species.

Keywords: Venomics; Snake venom; Venom proteomics; Snake Venomics Display; Visualization of venomics data, Snake venomics

Introduction

Venom proteomics has gained increasing attention in the last decade due to scientific interests in venom compositions, venom/toxin evolution, and elucidation of pathophysiological mechanisms of envenomings, as well as technological advances within proteomics and mass spectrometry that have allowed researchers to perform ever more in-depth investigations. In addition to venomics (Calvete, 2014), new fields have recently emerged, such as quantitative venomics, antivenomics, and functional venomics/toxicovenomics (Calvete, 2010; Calvete et al., 2017, 2009; Calvete and Lomonte, 2015; Laustsen, 2016; Laustsen et al., 2015a, 2015b; Lomonte and Calvete, 2017). Particularly within snake venomics, this has created a wealth of data that allows researchers to obtain a deeper understanding of venom function(s), evolutionary strategies for defense and prey subduction, and for developing improved antivenoms (Laustsen, n.d.; Laustsen et al., 2015a). However, with increasing complexity, a need for better structure and visualization of data presents itself. Inspired by how DNA and protein sequences are often visualized by linear alignment, and to alleviate the need for a database containing snake venomics data (Tasoulis and Isbister, 2017), we gathered all reported snake venomics data and created an Open Access visualization toolbox that is freely available to be used online. This toolbox, coined Snake Venomics Display, may help researchers obtain an overview of venom compositions within snake families, genera, and species, as well as guide scientist and physicians to quickly determine which toxin families are abundant in a given snakebite. This may be useful in the interpretation of large sets of venomics data, and it may aid the development of new antivenoms. Additionally, we have made all the venomics data included in our online database freely available in an Excel format by direct download via a link in the Snake Venomics Display toolbox.

Methods

Data collection

Data on toxin abundances was retrieved for 232 venom proteomes and for 10 venom gland transcriptomes (identified by a superscripted asterix in the snake name) from 143 snake species characterized in 103 original articles reviewed by Calvete (Calvete, 2013), Laustsen et al. (Laustsen et al., 2016), and Tasoulis & Isbister (Tasoulis and Isbister, 2017), and an online database was created. Abundances for trace toxins were consistently set to the maximum value of the interval (e.g. an abundance reported as <0.1% was set to 0.1% in our database). Venom yields were obtained from http://snakedatabase.org/ for the 83 species for which this information was available. In cases where the total venom abundance (in %) exceeded 100%, the data was normalized. All included venomics data is available in an Excel format by direct download in the Snake Venomics Display toolbox.

Building the program

The program was designed using the WordPress plugin: "wpDataTables". This plugin is widely used for its table-generation feature, and it possesses highly customizable charting functionalities used for the Snake Venomics Display toolbox. The venomics database described above was loaded into the plugin, and filters were specified with user-friendliness and functionality in mind. The data was then loaded in the plugin's "HighCharts" rendering software to display an interactive horizontal bar chart. Important functions, like responsiveness and setting the chart to follow the filter, were activated. A color scheme was manually defined so that colors express the protein family of the toxins. Visual specifications for the chart, such as units for axes and numbers, size, and credits link, were set, and the chart was embedded on the webpage. The same procedure was executed for both Snake Venomics Display visualization modes (Relative Abundance and Absolute Abundance).

Results and discussion

How to use the Snake Venomics Display toolbox

Upon loading the Snake Venomics Display toolbox at https://tropicalpharmacology.com/tools/snake-venomics-display/, a small description of the two currently available visualization modes (Relative Abundance and Absolute Abundance) is displayed together with buttons to access these modes (Figure 1). By clicking on one of these buttons, the user can use a tool in the Snake Venomics Display toolbox. The toolbox is by default filtered to display all venomics data available. However, the displayed snakes can be modified using the filtering system below the chart. Here, seven settings can be modified: "Snake" (name in Latin), "Common names" (in English), "Genus", "Family", "Country", "Region", and "Venom yield". The latter allows the user to only display data on snake venoms that have venom yields in a specified range (in mg). Venom yield data was retrieved from http://snakedatabase.org/. "Region" allows the user to select a region from which a desired snake or group of snakes are endemic. The snakes have been put into regions according to http://www.toxinology.com/. Searching for a country in the "Country" filter will display all snakes endemic in that specific country. "Family" allows the user to define which snake family to look at. "Genus" allows for filtering on the genus level, while "Latin name" can both filter for genus as well as a specific snake species. The "Common names" filter will display the venom compositions for snakes with a given common name. The common names have been acquired from http://www.toxinology.com/. The "Snake" filter is modified by typing the desired snake species or genus using Latin names, while "Common names" is modified by typing the desired common name of a species in English. "Country" and "Region" are applied similarly by typing the desired region and/or country. "Genus" and "Family" are specified using a drop-down menu. To remove the current filter and display all snakes in the database, the "CLEAR FILTERS" button is clicked. By clicking on the snake name, the user will be taken to the PubMed entry of the original publication from which

110 the data was collected. Finally, an “add data by request” button is provided to allow users to submit
111 their own published venomics data to help keep the database up to date.
112
113 **Relative venom compositions**
114 The Snake Venomics Display toolbox enables easy comparison of snake venoms by linear
115 visualization of venomics data. By selecting the Relative Abundance Display, the user will be able to
116 compare relative venom compositions (toxin family abundances expressed as percent of whole
117 venom) for families, genera, and species of snakes from different regions of the world. This can be
118 useful for quickly obtaining an overview of which toxin families are dominant in a given snake venom
119 and how this compares with closely and/or distantly related species. It is envisioned that this may be
120 particularly useful for researchers who wish to compare venoms from many snake species in relation
121 to snake venom evolution.
122 As an example, the relative abundance of toxin families present in venoms from the
123 Bitis genus can be seen in Figure 2. From this visualization, it quickly becomes evident that the Bitis
124 venoms share a similar relative venom composition, although *Bitis caudalis* distinguishes itself by
125 having a much higher proportion PLA_2s (purple).
126 In comparison with the similar, yet clearly different venom compositions of the Bitis
127 genus, the venom compositions for four selected Naja venoms are clearly more similar in terms of
128 relative abundance of toxin families (Figure 3). However, as these snake species are reported to
129 deliver very different venom yields when milked, the clinical manifestations may differ between bites
130 from different species within the genus. To visualize venom compositions in closer relation to the
131 possible medical impact that a bite from a given snake species may have, the Absolute Abundance
132 visualization mode was developed.
133

Absolute venom compositions

The Absolute Abundance visualization mode was developed to take venom yields into account when displaying venomics data. This represents a simple way of observing venom compositions, which may possibly provide a slightly more reliable indication of which toxin families are most medically relevant for a given envenoming case. As an example of this visualization mode, the same venoms from the Bitis genus are displayed in Figure 4. Here, it quickly becomes evident that even though *B. caudalis* venom is dominated by PLA_2s, this toxin family is more likely to have an actual medical impact in bites from the *Bitis gabonica* species due to the insignificant venom yields delivered by *B. caudalis* and the high venom yields delivered by *B. gabonica*.

Similarly, a very different picture emerges when comparing the previously selected Naja venoms in the Absolute Abundance visualization mode (Figure 5). Although bites from all four snake species should be handled as critical medical emergencies, it seems evident that severe bites from *Naja mossambica* can be more serious than bites from the other species.

A word of caution needs to be highlighted. Although the Absolute Abundance visualization mode may seem useful for evaluating the medical impact of bites from different snake species, this should in no case be used uncritically. Snakebites differ significantly, not only between species, but also between different specimens, with larger specimens being able to deliver larger amounts of venom in a bite. The Absolute Abundance visualization mode should thus mainly be used to provide a general overview of the *possible* severity of bites from different snake species – conceivably in introductory educational settings.

Conclusions

Snake Venomics Display is a toolbox for linear visualization of snake venomics data, which allows for better comparison of large sets of snake venom proteomes. This toolbox will be continuously improved for user-friendliness, as well as it will be updated with venomics data as this becomes

158 available. We invite researchers in the field to submit both such data as well as comments and
159 feedback, which we can use to make the Snake Venomics Display toolbox even more useful.
160

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165

166 ## Author contributions

167 A.H.L. conceived the study. S.D.P. collected the data. S.H.D., R.U.W.F., and A.M.E. designed and
168 developed the program. S.H.D. and R.U.W.F. analyzed the case data presented in the manuscript.
169 A.H.L., S.D.P., S.H.D., and R.U.W.F. wrote the manuscript. All authors reviewed the manuscript.

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Figure legends

Figure 1. Initial view upon loading the Snake Venomics Display toolbox (https://tropicalpharmacology.com/tools/snake-venomics-display/).

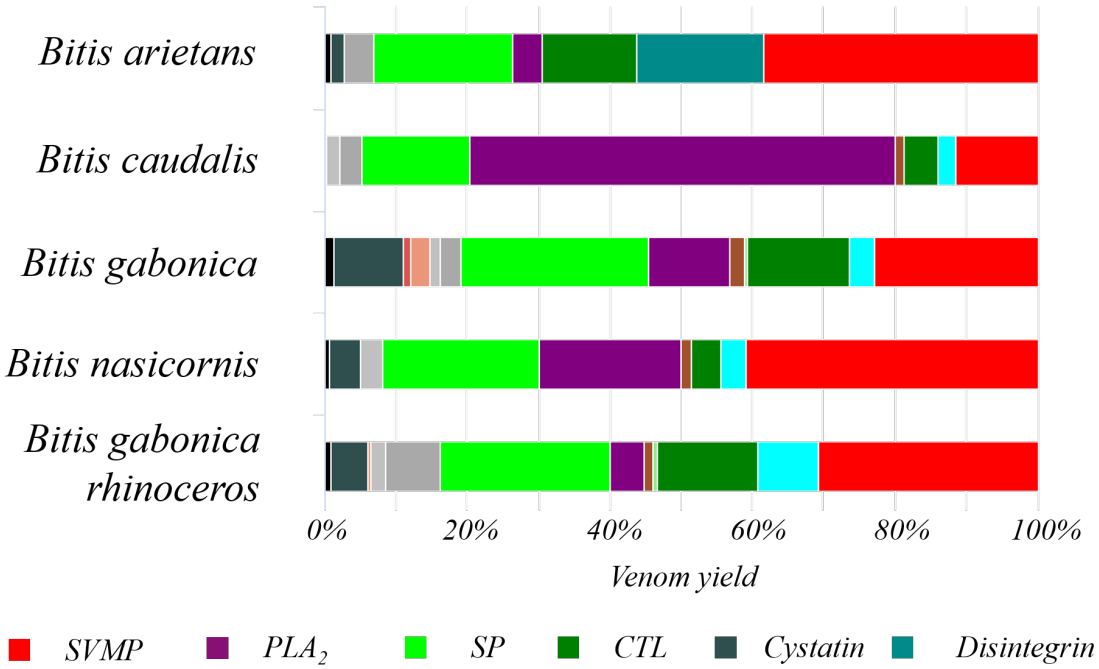


Figure 2. Display of the relative composition of selected venoms from the Bitis genus. Abbreviations: SVMP: Snake Venom MetalloProteinase. PLA_2: PhosphoLipase A2. SP: Serine Proteinase. CTL: C-Type Lectin.

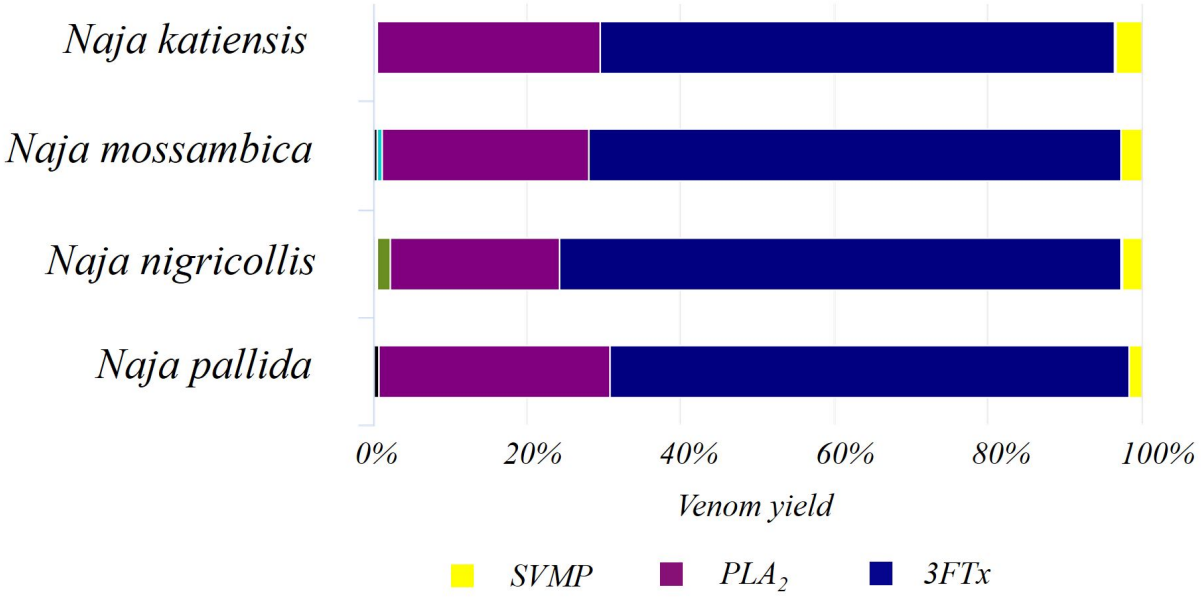
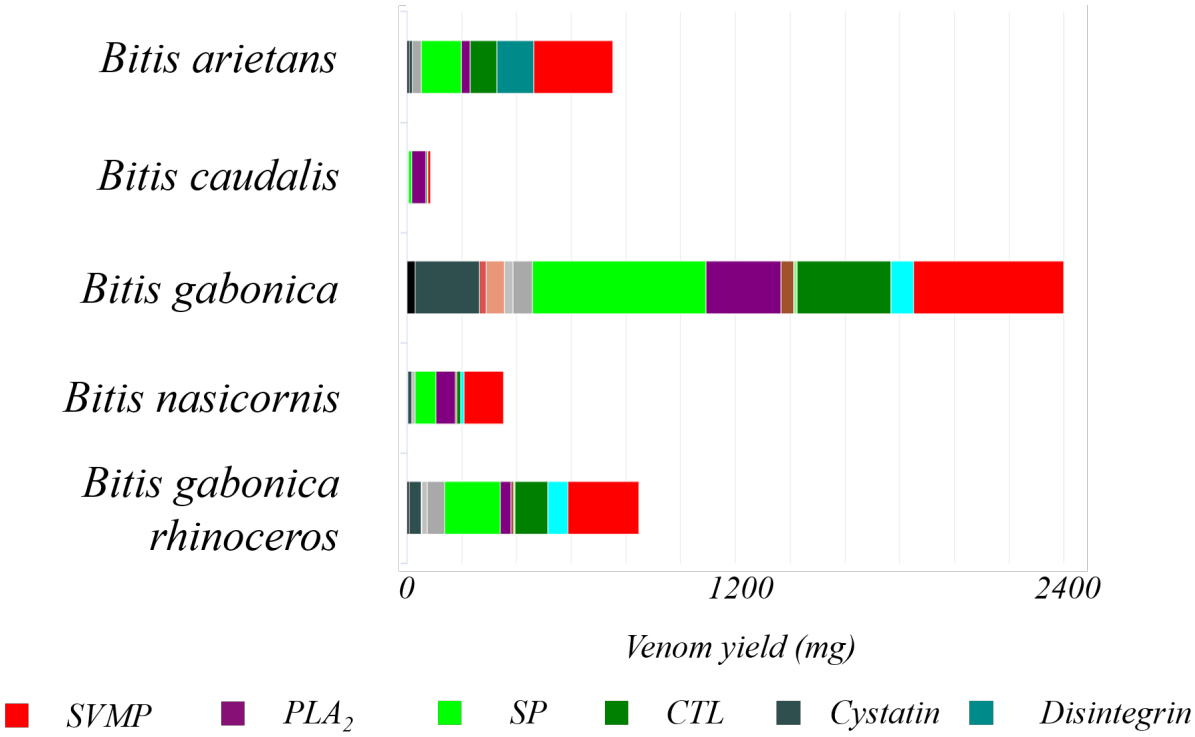


Figure 3. Display of the relative compositions of selected venoms from the Naja genus. Abbreviations: SVMP: Snake Venom Metalloproteinases. PLA_2: Phospholipases A_2. 3FTx: Three-Finger Toxins.



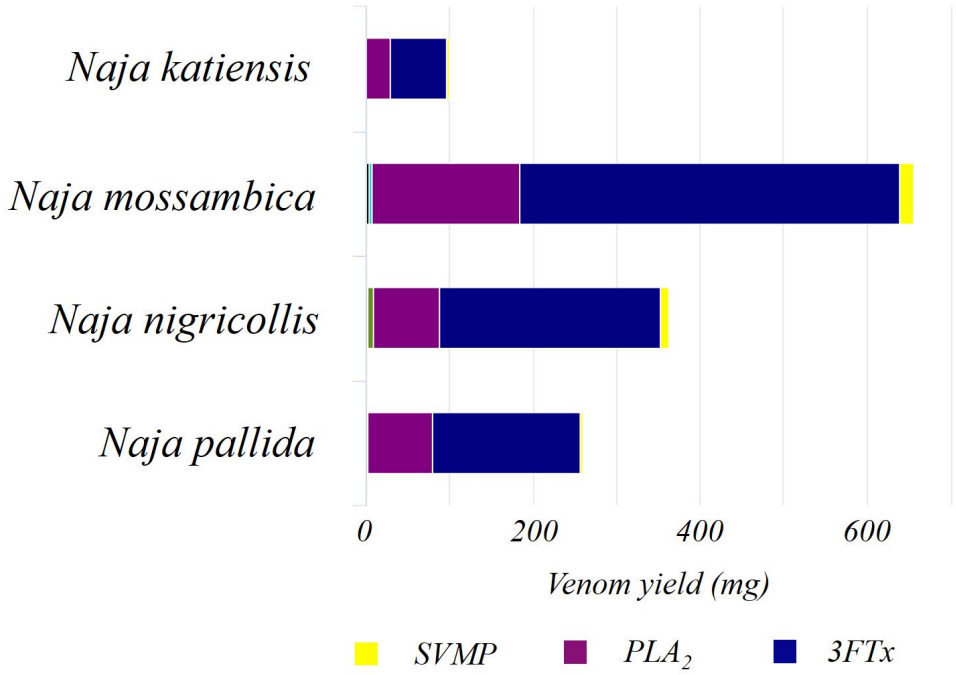
227

228 **Figure 4.** Display of the absolute compositions of selected venoms from the Bitis genus.

229 Abbreviations: SVMP: Snake Venom Metalloproteinase. PLA_2: Phospholipases A_2. SP: Serine

230 Proteinases. CTL: C-Type Lectins.

231



232

233 **Figure 5.** Display of the absolute compositions of selected venoms from the Naja genus.

234 Abbreviations: SVMP: Snake Venom Metalloproteinases. PLA_2: Phospholipases A_2. 3FTx: Three-

235 Finger Toxins.

236

237